

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43033 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-GTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGC-3' (SEQ ID NO:383).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO704 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO704 [herein designated as UNQ368 (DNA50911-1288)] (SEQ ID NO:379) and the derived protein sequence for PRO704.

The entire nucleotide sequence of UNQ368 (DNA50911-1288) is shown in Figure 152 (SEQ ID NO:379). Clone UNQ368 (DNA50911-1288) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 8-10 and ending at the stop codon at nucleotide positions 1052-1054 (Figure 152). The predicted polypeptide precursor is 348 amino acids long (Figure 153). The full-length PRO704 protein shown in Figure 153 has an estimated molecular weight of about 39,711 and a pI of about 8.7. Clone UNQ368 (DNA50911-1288) has been deposited with the ATCC on March 31, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO704 polypeptide suggests that portions of it possess significant homology to the vesicular integral membrane protein 36, thereby indicating that PRO704 may be a novel vesicular integral membrane protein.

Still analyzing the amino acid sequence of SEQ ID NO:380, the putative signal peptide is at about amino acids 1-39 of SEQ ID NO:380. The transmembrane domain is at amino acids 310-335 of SEQ ID NO:380. A potential N-glycosylation site is at about amino acids 180-183 of SEQ ID NO:380. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 60: Isolation of cDNA Clones Encoding Human PRO706

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA40669. Based on the DNA40669 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO706.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCAAGCAGCTTAGAGCTCCAGACC-3' (SEQ ID NO:386)

reverse PCR primer 5'-TTCCCTATGCTCTGTATTGGCATGG-3' (SEQ ID NO:387)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40669 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACTTCTGCCACAATGTCAGCTTTCCTGTACCAGAAATGGCTGTGTT-3' (SEQ ID NO:388)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO706 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO706 [herein designated as UNQ370 (DNA48329-1290)] (SEQ ID NO:384) and the derived protein sequence for PRO706. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

The entire nucleotide sequence of UNQ370 (DNA48329-1290) is shown in Figure 154 (SEQ ID NO:384). Clone UNQ370 (DNA48329-1290) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 279-281 and ending at the stop codon at nucleotide positions 1719-1721 (Figure 154). The predicted polypeptide precursor is 480 amino acids long (Figure 155). The full-length PRO706 protein shown in Figure 155 has an estimated molecular weight of about 55,239 daltons and a pI of about 9.30. Clone UNQ370 (DNA48329-1290) has been deposited with the ATCC on April 21, 1998.

Still regarding the amino acid sequence shown in Figure 155, there is a potential signal peptide cleavage site at about amino acid 19. There are potential N-glycosylation sites at about amino acid positions 305 and 354. There is a potential tyrosine kinase phosphorylation site at about amino acid position 333. A region homologous with histidine acid phosphatase is at about residues 87-102. The corresponding nucleic acid regions can be routinely determined given the provided sequences, i.e., the codons can be determined from the specifically named amino acids given.

Analysis of the amino acid sequence of the full-length PRO706 polypeptide suggests that portions of it possess significant homology to the human prostatic acid phosphatase precursor thereby indicating that PRO706 may be a novel human prostatic acid phosphatase.

#### EXAMPLE 61: Isolation of cDNA Clones Encoding Human PRO707

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42775. Based on DNA42775, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO707.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TCCGTCTCTGTGAACCGCCCCAC-3' (SEQ ID NO:391);

reverse PCR primer 5'-CTCGGGCGCATGTGCTTCTGGTC-3' (SEQ ID NO:392).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42775 sequence which had the following nucleotide sequence:

hybridization probe

5'-CCGACTGTGAAAGAGAACGCCCCAGATCCACTTATCCCC-3' (SEQ ID NO:393).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to

isolate clones encoding the PRO707 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO707 [herein designated as UNQ371 (DNA48306-1291)] (SEQ ID NO:389) and the derived protein sequence for PRO707.

The entire nucleotide sequence of UNQ371 (DNA48306-1291) is shown in Figure 156 (SEQ ID NO:389). Clone UNQ371 (DNA48306-1291) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 371-373 and ending at the stop codon at nucleotide positions 3119-3121 of SEQ ID NO:389. The predicted polypeptide precursor is 916 amino acids long (Figure 157). The full-length PRO707 protein shown in Figure 157 has an estimated molecular weight of about 100,204 daltons and a pI of about 4.92. Clone UNQ371 (DNA48306-1291) has been deposited with ATCC on May 27, 1998. It is understood that the clone UNQ371 which is deposited is that which encodes PRO707, and that the sequences herein are merely representations based on known sequencing techniques which may be subject to minor errors.

Regarding analysis of the amino acid sequence, the signal sequence appears to be at about 1 through 30 of SEQ ID NO:390. Cadherins extracellular repeated domain signature sequence is at about amino acids 121-131, 230-240, 335-345, 440-450, and 550-560 of SEQ ID NO:390. Tyrosine kinase phosphorylation sites are at about amino acids 124-132 and 580-586 of SEQ ID NO:390. A potential transmembrane domain is at about amino acids 682-715  $\pm$  5. The nucleic acid positions can be derived by referring to the corresponding codon for the named amino acid.

Analysis of the amino acid sequence of the full-length PRO707 polypeptide suggests that portions of it possess significant homology to the cadherin FIB3 protein, expressed in human fibroblasts, thereby indicating that PRO707 may be a novel cadherin.

#### EXAMPLE 62: Isolation of cDNA Clones Encoding Human PRO322

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA48336. Based on the DNA48336 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO322.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCCTACAGAATAAGATGGCCC-3' (SEQ ID NO:396)

reverse PCR primer 5'-GGTGCAATGATCTGCCAGGCTGAT-3' (SEQ ID NO:397)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA48336 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-AGAAATACCTGTGGITCAGTCCATCCCAAACCCCTGCTACAACAGCAG-3' (SEQ ID NO:398).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO322 gene using the probe oligonucleotide and one of the PCR primers. RNA